

SEQUENCE LISTING

<110> TOMLINSON, Stephen
HOLERS, V. Michael

<120> Complement Receptor 2 Targeted
Complement Modulators

<130> 577712000200

<140> US 10/534,772

<141> 2003-11-13

<150> PCT/US2003/036459

<151> 2003-11-13

<150> US 60/426,676

<151> 2002-11-15

<160> 29

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1041

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 1

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tttcccagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 120
gagaaggact cagtgatctg ccttaagggc agtcaatggt cagatattga agagttctgc 180
aatcgtagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 240
actcagaatt attttccagt cggtagctgt gtggaatatg agtgccgtcc aggttacaga 300
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 360
gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaaa tggtcagatt 420
gatgtaccag gtggcatatt atttggtgca accatctcct tctcatgtaa cacagggtac 480
aaattatttg gctcgacttc tagtttttgt cttatttcag gcagctctgt ccagtggagt 540
gacccgttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 600
ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta tgcattgta 660
aaaggattca ccatgattgg agagcaactct atttattgta ctgtgaataa tgatgaagga 720
gagtggagtg gccaccacc tgaatgcaga ggaaaatctc taacttccaa ggtcccacca 780
acagttcaga aacctaccac agtaaatggt ccaactacag aagtctcacc aacttctcag 840
aaaaccacca caaaaaccac cacaccaaat gctcaagcaa cacggagtac acctgtttcc 900
aggacaacca agcattttca tgaacaacc ccaaataaag gaagtggaa cacttcaggt 960
actaccgctc ttctatctgg gcacacgtgt ttcacgttga caggtttgct tgggacgcta 1020
gtaaccatgg gcttgctgac t 1041
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<210> 2

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 2

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Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly
 1          5          10          15
Glu Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val
          20          25          30
Trp Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu
          35          40          45
Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys
          50          55          60
Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys
65          70          75          80
Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser
          85          90          95
Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr
          100          105          110
Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys
          115          120          125
Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys
          130          135          140
Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Lys
145          150          155          160
Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro
          165          170          175
Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly
          180          185          190
Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser
          195          200          205
Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys
          210          215          220
Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp
225          230          235          240
His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe
          245          250          255
Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu
          260          265          270
Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr
          275          280          285
Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro
          290          295          300
Thr Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr Thr
305          310          315          320
Thr Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr
          325          330          335
Lys His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser
          340          345          350
Gly Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly
          355          360          365
Leu Leu Gly Thr Leu Val Thr Met Gly Leu Leu Thr
          370          375          380
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<210> 3

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 3
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gattttgatg cgtgtctcat taccaaagct gggttacaag tgtataacaa gtgttggaag 120
tttgagcatt gcaatttcaa cgacgtcaca acccgcttga gggaaaatga gctaacgtac 180
tactgtcgca agaaggacct gtgtaacttt aacgaacagc ttgaaaatgg tgggacatcc 240
ttatcagaga aaacagttct tctgctgggtg actccatttc tggcagcagc ctggagcctt 300
catccc 306

<210> 4
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 4
Met Gly Ile Gln Gly Gly Ser Val Leu Phe Gly Leu Leu Leu Val Leu
1 5 10 15
Ala Val Phe Cys His Ser Gly His Gln Cys Tyr Asn Cys Pro Asn Pro
20 25 30
Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe Asp Ala
35 40 45
Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys
50 55 60
Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg Glu Asn
65 70 75 80
Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu
85 90 95
Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys Thr Val Leu Leu
100 105 110
Leu Val Thr Pro Phe Leu Ala Ala Ala Trp Ser Leu His Pro
115 120 125

<210> 5
<211> 1485
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 5
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aaaagtcatt tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 180
aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtacc aggaggatac 240
aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 300
aacttctcca tgaacggaaa caagtctggt tgggtgcaag caaataatat gtgggggccc 360
acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc 420
cacaatggac atcacacaag tgagaatggt ggctccattg ctccaggatt gtctgtgact 480
tacagctgtg aatctggtta cttgcttggt ggagaaaaga tcattaactg tttgtcttcg 540
ggaaaatgga gtgctgtccc ccccatgtgt gaagaggcac gctgtaaact tctaggacga 600
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaaactt 660
ttctgtgatg aagggtatcg actgcaaggc ccaccttcta gtcggtgtgt aattgctgga 720
cagggagttg cttggacca aatgccagta tgtggaggtg ggtcgggtgg cggcgatcc 780
gactgtggcc ttccccaga tgtacctaat gccagccag ctttggaagg ccgtacaagt 840
tttcccgagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 900

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gagaaggact cagtgatctg ccttaagggc agtcaatggc cagatattga agagttctgc 960
aatcgtagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 1020
actcagaatt attttcagct cggtagctgt gtggaatatg agtgccgtcc aggttacaga 1080
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 1140
gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaaa tggtcagatt 1200
gatgtaccag gtggcatatt atttggtgca accatctcct tctcatgtaa cacagggtag 1260
aaattatttg gctcgacttc tagtttttgt cttatttcag gcagctctgt ccagtggagt 1320
gacccgttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 1380
ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta tgcattgta 1440
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```

<210> 6
<211> 495
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:/note =
        synthetic construct

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<400> 6
Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr
 1          5          10          15
Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser
          20          25          30
Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys
          35          40          45
Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr
          50          55          60
Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr
          65          70          75          80
Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe
          85          90          95
Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys
          100          105          110
Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser
          115          120          125
Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His
          130          135          140
His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr
          145          150          155          160
Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn
          165          170          175
Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu
          180          185          190
Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu
          195          200          205
Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu
          210          215          220
Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys Val Ile Ala Gly
          225          230          235          240
Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Gly Gly Gly Ser Gly
          245          250          255
Gly Gly Gly Ser Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln
          260          265          270
Pro Ala Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr
          275          280          285
Tyr Lys Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser
          290          295          300
Val Ile Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys
          305          310          315          320

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Asn	Arg	Ser	Cys	Glu	Val	Pro	Thr	Arg	Leu	Asn	Ser	Ala	Ser	Leu	Lys
				325					330					335	
Gln	Pro	Tyr	Ile	Thr	Gln	Asn	Tyr	Phe	Pro	Val	Gly	Thr	Val	Val	Glu
			340					345					350		
Tyr	Glu	Cys	Arg	Pro	Gly	Tyr	Arg	Arg	Glu	Pro	Ser	Leu	Ser	Pro	Lys
		355					360					365			
Leu	Thr	Cys	Leu	Gln	Asn	Leu	Lys	Trp	Ser	Thr	Ala	Val	Glu	Phe	Cys
	370					375					380				
Lys	Lys	Lys	Ser	Cys	Pro	Asn	Pro	Gly	Glu	Ile	Arg	Asn	Gly	Gln	Ile
	385				390					395					400
Asp	Val	Pro	Gly	Gly	Ile	Leu	Phe	Gly	Ala	Thr	Ile	Ser	Phe	Ser	Cys
			405						410					415	
Asn	Thr	Gly	Tyr	Lys	Leu	Phe	Gly	Ser	Thr	Ser	Ser	Phe	Cys	Leu	Ile
		420					425					430			
Ser	Gly	Ser	Ser	Val	Gln	Trp	Ser	Asp	Pro	Leu	Pro	Glu	Cys	Arg	Glu
	435					440					445				
Ile	Tyr	Cys	Pro	Ala	Pro	Pro	Gln	Ile	Asp	Asn	Gly	Ile	Ile	Gln	Gly
	450				455						460				
Glu	Arg	Asp	His	Tyr	Gly	Tyr	Arg	Gln	Ser	Val	Thr	Tyr	Ala	Cys	Asn
	465			470						475					480
Lys	Gly	Phe	Thr	Met	Ile	Gly	Glu	His	Ser	Ile	Tyr	Cys	Thr	Val	
				485				490						495	

<210> 7
 <211> 1002
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 7
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 attgctgttg gtaccgtgat aaggtagcgt tgttcaggta ccttccgcct cattggagaa 120
 aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 180
 aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtacc aggaggatac 240
 aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 300
 aacttctcca tgaacggaaa caagtctgtt tgggtgtcaag caaataatat gtgggggccc 360
 acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc 420
 cacaatggac atcacacaag tgagaatgtt ggctccattg ctccaggatt gtctgtgact 480
 tacagctgtg aatctgggta cttgcttgtt ggagaaaaga tcattaactg tttgtcttcg 540
 ggaaaatgga gtgctgtccc ccccatatgt gaagaggcac gctgtaaatc tctaggacga 600
 tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaacttt 660
 ttctgtgatg aagggtatcg actgcaaggc ccaccttcta gtcggtgtgt aattgctgga 720
 caggaggttg cttggaccaa aatgccagta tgttcaggag gaggagggtc cctgcagtgc 780
 tacaactgtc ctaaccacaa tgctgactgc aaaacagccg tcaattgttc atctgatttt 840
 gatgcgtgtc tcattaccaa agctgggtta caagtgtata acaagtgttg gaagtttgag 900
 cattgcaatt tcaacgacgt cacaaccgcg ttgagggaaa atgagctaac gtactactgc 960
 tgcaagaagg acctgtgtaa ctttaacgaa cagcttgaaa at 1002

<210> 8
 <211> 334
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 8

Ile	Ser	Cys	Gly	Ser	Pro	Pro	Pro	Ile	Leu	Asn	Gly	Arg	Ile	Ser	Tyr
1				5					10					15	
Tyr	Ser	Thr	Pro	Ile	Ala	Val	Gly	Thr	Val	Ile	Arg	Tyr	Ser	Cys	Ser
			20					25					30		
Gly	Thr	Phe	Arg	Leu	Ile	Gly	Glu	Lys	Ser	Leu	Leu	Cys	Ile	Thr	Lys
		35				40					45				
Asp	Lys	Val	Asp	Gly	Thr	Trp	Asp	Lys	Pro	Ala	Pro	Lys	Cys	Glu	Tyr
	50					55					60				
Phe	Asn	Lys	Tyr	Ser	Ser	Cys	Pro	Glu	Pro	Ile	Val	Pro	Gly	Gly	Tyr
65				70						75				80	
Lys	Ile	Arg	Gly	Ser	Thr	Pro	Tyr	Arg	His	Gly	Asp	Ser	Val	Thr	Phe
				85					90					95	
Ala	Cys	Lys	Thr	Asn	Phe	Ser	Met	Asn	Gly	Asn	Lys	Ser	Val	Trp	Cys
			100					105					110		
Gln	Ala	Asn	Asn	Met	Trp	Gly	Pro	Thr	Arg	Leu	Pro	Thr	Cys	Val	Ser
		115				120						125			
Val	Phe	Pro	Leu	Glu	Cys	Pro	Ala	Leu	Pro	Met	Ile	His	Asn	Gly	His
	130					135					140				
His	Thr	Ser	Glu	Asn	Val	Gly	Ser	Ile	Ala	Pro	Gly	Leu	Ser	Val	Thr
145				150						155				160	
Tyr	Ser	Cys	Glu	Ser	Gly	Tyr	Leu	Leu	Val	Gly	Glu	Lys	Ile	Ile	Asn
				165					170					175	
Cys	Leu	Ser	Ser	Gly	Lys	Trp	Ser	Ala	Val	Pro	Pro	Thr	Cys	Glu	Glu
			180					185					190		
Ala	Arg	Cys	Lys	Ser	Leu	Gly	Arg	Phe	Pro	Asn	Gly	Lys	Val	Lys	Glu
		195				200						205			
Pro	Pro	Ile	Leu	Arg	Val	Gly	Val	Thr	Ala	Asn	Phe	Phe	Cys	Asp	Glu
		210				215						220			
Gly	Tyr	Arg	Leu	Gln	Gly	Pro	Pro	Ser	Ser	Arg	Cys	Val	Ile	Ala	Gly
225				230						235				240	
Gln	Gly	Val	Ala	Trp	Thr	Lys	Met	Pro	Val	Cys	Ser	Gly	Gly	Gly	Gly
				245					250					255	
Ser	Leu	Gln	Cys	Tyr	Asn	Cys	Pro	Asn	Pro	Thr	Ala	Asp	Cys	Lys	Thr
			260					265					270		
Ala	Val	Asn	Cys	Ser	Ser	Asp	Phe	Asp	Ala	Cys	Leu	Ile	Thr	Lys	Ala
		275					280						285		
Gly	Leu	Gln	Val	Tyr	Asn	Lys	Cys	Trp	Lys	Phe	Glu	His	Cys	Asn	Phe
		290				295					300				
Asn	Asp	Val	Thr	Thr	Arg	Leu	Arg	Glu	Asn	Glu	Leu	Thr	Tyr	Tyr	Cys
305					310					315					320
Cys	Lys	Lys	Asp	Leu	Cys	Asn	Phe	Asn	Glu	Gln	Leu	Glu	Asn		
				325					330						

<210> 9

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 9

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gactgtggcc ttccccaga tgtacctaat gccagccag ctttggagg ccgtacaagt 60
tttcccaggg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 120
gagaaggact cagtgatctg ccttaagggc agtcaatggt cagatattga agagttctgc 180
aatcgtagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 240
actcagaatt attttccagt cggtactgtt gtggaatatg agtgccgtcc aggttacaga 300
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 360

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gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaaa tggtcagatt 420
gatgtaccag gtggcatatt atttgggtgca accatctcct tctcatgtaa cacaggggtac 480
aaattatttg gctcgacttc tagtttttgt cttatttcag gcagctctgt ccagtggagt 540
gacccgttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 600
ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta tgcattgta 660
aaaggattca ccatgattgg agagcactct atttattgta ctgtgaataa tgatgaagga 720
gagtggagtg gcccaccacc tgaatgcaga tcctctgggtg gcggtggctc gggcggaggt 780
gggtcgggtg gcggcggatc catttcttgt ggctctcctc cgctatcct aaatggccgg 840
attagttatt attctacccc cattgctgtt ggtaccgtga taaggtagag ttgttcaggt 900
accttccgcc tcattggaga aaaaagtcta ttatgcataa ctaaaagaaa agtggatgga 960
acctgggata aacctgctcc taaatgtgaa tatttcaata aatattcttc ttgccctgag 1020
cccatagtag caggaggata caaaattaga ggctctacac cctacagaca tggtagattct 1080
gtgacatttg cctgtaaaac caacttctcc atgaacggaa acaagtctgt ttggtgtcaa 1140
gcaaataata tgtggggggc gacacgacta ccaacctgtg taagtgtttt ccctctcgag 1200
tgtccagcac ttcctatgat ccacaatgga catcacacia gtgagaatgt tggctccatt 1260
gctccaggat tgtctgtgac ttacagctgt gaatctggtt acttgcttgt tggagaaaag 1320
atcattaact gtttgtcttc gggaaaatgg agtgctgtcc cccccacatg tgaagaggca 1380
cgctgtaaat ctctaggacg atttcccaat gggaaggtaa aggagcctcc aattctccgg 1440
gttggtgtaa ctgcaaacct tttctgtgat gaagggtatc gactgcaagg cccaccttct 1500
agtcggtgtg taattgctgg acagggagtt gcttggacca aaatgccagt atgt 1554

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<210> 10

<211> 518

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =

synthetic construct

<400> 10

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Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu
 1             5             10             15
Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu
          20          25          30
Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys Leu
          35          40          45
Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys
          50          55          60
Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile
          65          70          75          80
Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg
          85          90          95
Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu
          100          105          110
Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Ser
          115          120          125
Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro Gly
          130          135          140
Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly Tyr
          145          150          155          160
Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser Ser
          165          170          175
Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys Pro
          180          185          190
Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp His
          195          200          205
Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe Thr
          210          215          220
Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu Gly

```

225		230		235		240
Glu Trp Ser Gly Pro	Pro Pro Glu Cys Arg Ser Ser Gly Gly Gly Gly					
	245		250		255	
Ser Gly Gly Gly Gly	Ser Gly Gly Gly Gly Ser Ile Ser Cys Gly Ser					
	260		265		270	
Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr Tyr Ser Thr Pro Ile						
	275		280		285	
Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser Gly Thr Phe Arg Leu						
	290		295		300	
Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys Asp Lys Val Asp Gly						
305	310		315		320	
Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr Phe Asn Lys Tyr Ser						
	325		330		335	
Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr Lys Ile Arg Gly Ser						
	340		345		350	
Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe Ala Cys Lys Thr Asn						
	355		360		365	
Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys Gln Ala Asn Asn Met						
	370		375		380	
Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser Val Phe Pro Leu Glu						
385	390		395		400	
Cys Pro Ala Leu Pro Met Ile His Asn Gly His His Thr Ser Glu Asn						
	405		410		415	
Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr Tyr Ser Cys Glu Ser						
	420		425		430	
Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn Cys Leu Ser Ser Gly						
	435		440		445	
Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu Ala Arg Cys Lys Ser						
	450		455		460	
Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu Pro Pro Ile Leu Arg						
465	470		475		480	
Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu Gly Tyr Arg Leu Gln						
	485		490		495	
Gly Pro Pro Ser Ser Arg Cys Val Ile Ala Gly Gln Gly Val Ala Trp						
	500		505		510	
Thr Lys Met Pro Val Cys						
	515					

<210> 11
 <211> 990
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 11
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 aagtttgagc attgcaattt caacgacgtc acaaccgct tgagggaaaa tgagctaacy 180
 tactactgct gcaagaagga cctgtgtaac tttaacgaac agcttgaaaa ttcctctggt 240
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 ccgcctatcc taaatggccg gattagttat tattctaccc ccattgctgt tggtagcgtg 360
 ataaggtaca gttgttcagg taccttccgc ctcatggag aaaaaagtct attatgcata 420
 actaaagaca aagtggatgg aacctggat aaacctgctc cttaaagtga atatttcaat 480
 aaatattctt cttgccctga gcccatagta ccaggaggat acaaaattag aggctctaca 540
 ccctacagac atggtgattc tgtgacattt gcctgtaaaa ccaacttctc catgaacgga 600
 aacaagtctg tttggtgtca agcaaataat atgtgggggc cgacacgact accaactgt 660
 gtaagtgttt tccctctcga gtgtccagca cttcctatga tccacaatgg acatcacaca 720


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agtgagaatg ttggctccat tgctccagga ttgtctgtga cttacagctg tgaatctggt 780
tacttgcttg ttggagaaaa gatcattaac tgtttgtctt cgggaaaatg gagtgctgtc 840
ccccccacat gtgaagaggc acgctgtaaa tctctaggac gatttcccaa tgggaaggta 900
aaggagcctc caattctccg ggttggtgta actgcaaact ttttctgtga tgaagggtat 960
cgactgcaag gccaccttc tagtcggtgt 990

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<210> 12

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 12

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 1          5          10          15
Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
          20          25          30
Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
          35          40          45
Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
          50          55          60
Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Ser Ser Gly
65          70          75          80
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Ser
          85          90          95
Cys Gly Ser Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr Tyr Ser
          100          105          110
Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser Gly Thr
          115          120          125
Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys Asp Lys
          130          135          140
Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr Phe Asn
145          150          155          160
Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr Lys Ile
          165          170          175
Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe Ala Cys
          180          185          190
Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys Gln Ala
          195          200          205
Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser Val Phe
          210          215          220
Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His His Thr
225          230          235          240
Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr Tyr Ser
          245          250          255
Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn Cys Leu
          260          265          270
Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu Ala Arg
          275          280          285
Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu Pro Pro
          290          295          300
Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu Gly Tyr
305          310          315          320
Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
          325          330

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<210> 13

<211> 5994
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 13
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 ttttctatca tctgcctaaa aaactcagtc tggactgggtg ctaaggacag gtgcagacgt 180
 aaatcatgtc gtaatcctcc agatcctgtg aatggcatgg tgcattgtgat caaaggcatc 240
 cagttcggat cccaaattaa atattcttgt actaaaggat accgactcat tggttcctcg 300
 tctgccacat gcatcatctc aggtgatact gtcatttggg ataataaaaac acctatttgt 360
 gacagaattc cttgtgggct acccccacc atcaccaatg gagatttcat tagcaccaac 420
 agagagaatt ttcactatgg atcagtgggtg acctaccgtg gcaatcctgg aagcggaggg 480
 agaaagggtg ttgagcttgt gggtagagcc tccatatact gcaccagcaa tgacgatcaa 540
 gtgggcatct ggagcggccc cgccctcag tgcattatac ctaacaaatg cacgcctcca 600
 aatgtggaaa atggaatatt ggtatctgac aacagaagct tattttcctt aaatgaagtt 660
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<210> 14

<211> 2048

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 14

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Val	Gly	Pro	Pro	Ala	Pro	Gly	Leu	Pro	Phe	Cys	Cys	Gly	Gly	Ser	Leu
			20					25					30		
Leu	Ala	Val	Val	Val	Leu	Leu	Ala	Leu	Pro	Val	Ala	Trp	Gly	Gln	Cys
			35				40					45			
Asn	Ala	Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr
			50			55					60				
Asn	Leu	Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr
65				70						75				80	
Glu	Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu
				85					90					95	
Lys	Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser
			100					105					110		
Cys	Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys
			115				120					125			
Gly	Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr
			130				135					140			
Arg	Leu	Ile	Gly	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	
145				150					155					160	
Val	Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly
				165					170					175	
Leu	Pro	Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu
			180					185					190		
Asn	Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser
			195				200					205			
Gly	Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys
			210				215					220			
Thr	Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln
225					230					235					240
Cys	Ile	Ile	Pro	Asn	Lys	Cys	Thr	Pro	Pro	Asn	Val	Glu	Asn	Gly	Ile
				245					250					255	
Leu	Val	Ser	Asp	Asn	Arg	Ser	Leu	Phe	Ser	Leu	Asn	Glu	Val	Val	Glu
				260				265					270		
Phe	Arg	Cys	Gln	Pro	Gly	Phe	Val	Met	Lys	Gly	Pro	Arg	Arg	Val	Lys
			275				280					285			
Cys	Gln	Ala	Leu	Asn	Lys	Trp	Glu	Pro	Glu	Leu	Pro	Ser	Cys	Ser	Arg
			290				295				300				
Val	Cys	Gln	Pro	Pro	Pro	Asp	Val	Leu	His	Ala	Glu	Arg	Thr	Gln	Arg
305					310					315					320
Asp	Lys	Asp	Asn	Phe	Ser	Pro	Gly	Gln	Glu	Val	Phe	Tyr	Ser	Cys	Glu
				325					330					335	
Pro	Gly	Tyr	Asp	Leu	Arg	Gly	Ala	Ala	Ser	Met	Arg	Cys	Thr	Pro	Gln
			340				345						350		
Gly	Asp	Trp	Ser	Pro	Ala	Ala	Pro	Thr	Cys	Glu	Val	Lys	Ser	Cys	Asp
			355				360					365			
Asp	Phe	Met	Gly	Gln	Leu	Leu	Asn	Gly	Arg	Val	Leu	Phe	Pro	Val	Asn
			370			375					380				
Leu	Gln	Leu	Gly	Ala	Lys	Val	Asp	Phe	Val	Cys	Asp	Glu	Gly	Phe	Gln
385					390					395					400
Leu	Lys	Gly	Ser	Ser	Ala	Ser	Tyr	Cys	Val	Leu	Ala	Gly	Met	Glu	Ser
				405					410					415	
Leu	Trp	Asn	Ser	Ser	Val	Pro	Val	Cys	Glu	Gln	Ile	Phe	Cys	Pro	Ser
			420				425						430		
Pro	Pro	Val	Ile	Pro	Asn	Gly	Arg	His	Thr	Gly	Lys	Pro	Leu	Glu	Val
			435				440					445			
Phe	Pro	Phe	Gly	Lys	Ala	Val	Asn	Tyr	Thr	Cys	Asp	Pro	His	Pro	Asp
			450			455					460				
Arg	Gly	Thr	Ser	Phe	Asp	Leu	Ile	Gly	Glu	Ser	Thr	Ile	Arg	Cys	Thr
465					470					475					480
Ser	Asp	Pro	Gln	Gly	Asn	Gly	Val	Trp	Ser	Ser	Pro	Ala	Pro	Arg	Cys

Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser
980 985 990
Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys
995 1000 1005
Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val
1010 1015 1020
His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys
1025 1030 1035 1040
Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu
1045 1050 1055
Ser Gly Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg
1060 1065 1070
Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser
1075 1080 1085
Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys
1090 1095 1100
Asn Leu Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro
1105 1110 1115 1120
Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly
1125 1130 1135
Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val
1140 1145 1150
Glu Asn Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn
1155 1160 1165
Glu Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro
1170 1175 1180
Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro
1185 1190 1195 1200
Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu His Gly Glu
1205 1210 1215
His Thr Pro Ser His Gln Asp Asn Phe Ser Pro Gly Gln Glu Val Phe
1220 1225 1230
Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Leu His
1235 1240 1245
Cys Thr Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg Cys Ala Val
1250 1255 1260
Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu
1265 1270 1275 1280
Phe Pro Leu Asn Leu Leu Gly Ala Lys Val Ser Phe Val Cys Asp
1285 1290 1295
Glu Gly Phe Arg Leu Lys Gly Ser Ser Val Ser His Cys Val Leu Val
1300 1305 1310
Gly Met Arg Ser Leu Trp Asn Asn Ser Val Pro Val Cys Glu His Ile
1315 1320 1325
Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His Thr Gly Thr
1330 1335 1340
Pro Ser Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr Thr Cys Asp
1345 1350 1355 1360
Pro His Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly Glu Ser Thr
1365 1370 1375
Ile Arg Cys Thr Ser Asp Pro His Gly Asn Gly Val Trp Ser Ser Pro
1380 1385 1390
Ala Pro Arg Cys Glu Leu Ser Val Arg Ala Gly His Cys Lys Thr Pro
1395 1400 1405
Glu Gln Phe Pro Phe Ala Ser Pro Thr Ile Pro Ile Asn Asp Phe Glu
1410 1415 1420
Phe Pro Val Gly Thr Ser Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Phe
1425 1430 1435 1440
Gly Lys Met Phe Ser Ile Ser Cys Leu Glu Asn Leu Val Trp Ser Ser
1445 1450 1455
Val Glu Asp Asn Cys Arg Arg Lys Ser Cys Gly Pro Pro Pro Glu Pro

1460					1465					1470					
Phe	Asn	Gly	Met	Val	His	Ile	Asn	Thr	Asp	Thr	Gln	Phe	Gly	Ser	Thr
1475					1480					1485					
Val	Asn	Tyr	Ser	Cys	Asn	Glu	Gly	Phe	Arg	Leu	Ile	Gly	Ser	Pro	Ser
1490					1495					1500					
Thr	Thr	Cys	Leu	Val	Ser	Gly	Asn	Asn	Val	Thr	Trp	Asp	Lys	Lys	Ala
1505	1510					1515					1520				
Pro	Ile	Cys	Glu	Ile	Ile	Ser	Cys	Glu	Pro	Pro	Pro	Thr	Ile	Ser	Asn
1525					1530					1535					
Gly	Asp	Phe	Tyr	Ser	Asn	Asn	Arg	Thr	Ser	Phe	His	Asn	Gly	Thr	Val
1540					1545					1550					
Val	Thr	Tyr	Gln	Cys	His	Thr	Gly	Pro	Asp	Gly	Glu	Gln	Leu	Phe	Glu
1555					1560					1565					
Leu	Val	Gly	Glu	Arg	Ser	Ile	Tyr	Cys	Thr	Ser	Lys	Asp	Asp	Gln	Val
1570					1575					1580					
Gly	Val	Trp	Ser	Ser	Pro	Pro	Pro	Arg	Cys	Ile	Ser	Thr	Asn	Lys	Cys
1585	1590					1595					1600				
Thr	Ala	Pro	Glu	Val	Glu	Asn	Ala	Ile	Arg	Val	Pro	Gly	Asn	Arg	Ser
1605					1610					1615					
Phe	Phe	Ser	Leu	Thr	Glu	Ile	Ile	Arg	Phe	Arg	Cys	Gln	Pro	Gly	Phe
1620					1625					1630					
Val	Met	Val	Gly	Ser	His	Thr	Val	Gln	Cys	Gln	Thr	Asn	Gly	Arg	Trp
1635					1640					1645					
Gly	Pro	Lys	Leu	Pro	His	Cys	Ser	Arg	Val	Cys	Gln	Pro	Pro	Pro	Glu
1650					1655					1660					
Ile	Leu	His	Gly	Glu	His	Thr	Leu	Ser	His	Gln	Asp	Asn	Phe	Ser	Pro
1665	1670					1675					1680				
Gly	Gln	Glu	Val	Phe	Tyr	Ser	Cys	Glu	Pro	Ser	Tyr	Asp	Leu	Arg	Gly
1685					1690					1695					
Ala	Ala	Ser	Leu	His	Cys	Thr	Pro	Gln	Gly	Asp	Trp	Ser	Pro	Glu	Ala
1700					1705					1710					
Pro	Arg	Cys	Thr	Val	Lys	Ser	Cys	Asp	Asp	Phe	Leu	Gly	Gln	Leu	Pro
1715					1720					1725					
His	Gly	Arg	Val	Leu	Leu	Pro	Leu	Asn	Leu	Gln	Leu	Gly	Ala	Lys	Val
1730					1735					1740					
Ser	Phe	Val	Cys	Asp	Glu	Gly	Phe	Arg	Leu	Lys	Gly	Arg	Ser	Ala	Ser
1745	1750					1755					1760				
His	Cys	Val	Leu	Ala	Gly	Met	Lys	Ala	Leu	Trp	Asn	Ser	Ser	Val	Pro
1765					1770					1775					
Val	Cys	Glu	Gln	Ile	Phe	Cys	Pro	Asn	Pro	Pro	Ala	Ile	Leu	Asn	Gly
1780					1785					1790					
Arg	His	Thr	Gly	Thr	Pro	Phe	Gly	Asp	Ile	Pro	Tyr	Gly	Lys	Glu	Ile
1795					1800					1805					
Ser	Tyr	Ala	Cys	Asp	Thr	His	Pro	Asp	Arg	Gly	Met	Thr	Phe	Asn	Leu
1810					1815					1820					
Ile	Gly	Glu	Ser	Ser	Ile	Arg	Cys	Thr	Ser	Asp	Pro	Gln	Gly	Asn	Gly
1825	1830					1835					1840				
Val	Trp	Ser	Ser	Pro	Ala	Pro	Arg	Cys	Glu	Leu	Ser	Val	Pro	Ala	Ala
1845					1850					1855					
Cys	Pro	His	Pro	Pro	Lys	Ile	Gln	Asn	Gly	His	Tyr	Ile	Gly	Gly	His
1860					1865					1870					
Val	Ser	Leu	Tyr	Leu	Pro	Gly	Met	Thr	Ile	Ser	Tyr	Thr	Cys	Asp	Pro
1875					1880					1885					
Gly	Tyr	Leu	Leu	Val	Gly	Lys	Gly	Phe	Ile	Phe	Cys	Thr	Asp	Gln	Gly
1890					1895					1900					
Ile	Trp	Ser	Gln	Leu	Asp	His	Tyr	Cys	Lys	Glu	Val	Asn	Cys	Ser	Phe
1905	1910					1915					1920				
Pro	Leu	Phe	Met	Asn	Gly	Ile	Ser	Lys	Glu	Leu	Glu	Met	Lys	Lys	Val
1925					1930					1935					
Tyr	His	Tyr	Gly	Asp	Tyr	Val	Thr	Leu	Lys	Cys	Glu	Asp	Gly	Tyr	Thr

1940	1945	1950
Leu Glu Gly Ser Pro Trp Ser Gln Cys Gln Ala Asp Asp Arg Trp Asp		
1955	1960	1965
Pro Pro Leu Ala Lys Cys Thr Ser Arg Ala His Asp Ala Leu Ile Val		
1970	1975	1980
Gly Thr Leu Ser Gly Thr Ile Phe Phe Ile Leu Leu Ile Ile Phe Leu		
1985	1990	1995
Ser Trp Ile Ile Leu Lys His Arg Lys Gly Asn Asn Ala His Glu Asn		2000
2005	2010	2015
Pro Lys Glu Val Ala Ile His Leu His Ser Gln Gly Gly Ser Ser Val		
2020	2025	2030
His Pro Arg Thr Leu Gln Thr Asn Glu Glu Asn Ser Arg Val Leu Pro		
2035	2040	2045

<210> 15
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 15
 tgtgaggagc caccaacatt tgaagctatg gagctcattg gtaaaccaaa accctactat 60
 gagattggtg aacgagtaga ttataagtgt aaaaaaggat acttctatat acctcctctt 120
 gccacccata ctatttgtga tcggaatcat acatggctac ctgtctcaga tgacgcctgt 180
 tatagagaaa catgtccata tatacgggat cctttaaatg gccaaagcagt ccctgcaa 240
 gggacttacg agtttgggta tcagatgcac tttatttgta atgagggtta ttacttaatt 300
 ggtgaagaaa ttctatattg tgaacttaaa ggatcagtag caatttggag cggtaagccc 360
 ccaatatgtg aaaagggttt gtgtacacca cctccaaaaa taaaaaatgg aaaacacacc 420
 tttagtgaag tagaagtatt tgagtatctt gatgcagtaa cttatagttg tgatcctgca 480
 cctggaccag atccattttc acttattgga gagagcacga tttattgtgg tgacaattca 540
 gtgtggagtc gtgctgtccc agagtgtaaa gtggtcaaat gtcgatttcc agtagtcgaa 600
 aatggaaaac agatatcagg atttggaaaa aaattttact acaaagcaac agttatgttt 660
 gaatgcgata aggggtttta cctcgatggc agcgacacaa ttgtctgtga cagtaacagt 720
 acttgggatc cccagttcc aaagtgtcct aaagtgtcga cttcttccac tacaaaatct 780
 ccagcgtcca gtgctcagg tcctaggcct acttacaagc ctccagtctc aaattatcca 840
 ggatatccta aacctgagga aggaatactt gacagtgttg atgtttgggt cattgctgtg 900
 attgttattg ccatagttgt tggagttgca gtaatttgtg ttgtcccgtg cagatatctt 960
 caaaggagga agaagaaagg cacataccta actgatgaga cccacagaga agtaaaattt 1020
 acttctctc 1029

<210> 16
 <211> 378
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 16
 Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
 1 5 10 15
 Phe Pro Gly Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe
 20 25 30
 Ser Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile
 35 40 45
 Gly Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys

50						55					60					
Cys	Lys	Lys	Gly	Tyr	Phe	Tyr	Ile	Pro	Pro	Leu	Ala	Thr	His	Thr	Ile	
65					70					75					80	
Cys	Asp	Arg	Asn	His	Thr	Trp	Leu	Pro	Val	Ser	Asp	Asp	Ala	Cys	Tyr	
				85					90					95		
Arg	Glu	Thr	Cys	Pro	Tyr	Ile	Arg	Asp	Pro	Leu	Asn	Gly	Gln	Ala	Val	
			100					105					110			
Pro	Ala	Asn	Gly	Thr	Tyr	Glu	Phe	Gly	Tyr	Gln	Met	His	Phe	Ile	Cys	
		115					120					125				
Asn	Glu	Gly	Tyr	Tyr	Leu	Ile	Gly	Glu	Glu	Ile	Leu	Tyr	Cys	Glu	Leu	
	130					135					140					
Lys	Gly	Ser	Val	Ala	Ile	Trp	Ser	Gly	Lys	Pro	Pro	Ile	Cys	Glu	Lys	
145					150					155					160	
Val	Leu	Cys	Thr	Pro	Pro	Pro	Lys	Ile	Lys	Asn	Gly	Lys	His	Thr	Phe	
				165					170					175		
Ser	Glu	Val	Glu	Val	Phe	Glu	Tyr	Leu	Asp	Ala	Val	Thr	Tyr	Ser	Cys	
		180						185					190			
Asp	Pro	Ala	Pro	Gly	Pro	Asp	Pro	Phe	Ser	Leu	Ile	Gly	Glu	Ser	Thr	
	195						200					205				
Ile	Tyr	Cys	Gly	Asp	Asn	Ser	Val	Trp	Ser	Arg	Ala	Ala	Pro	Glu	Cys	
	210				215						220					
Lys	Val	Val	Lys	Cys	Arg	Phe	Pro	Val	Val	Glu	Asn	Gly	Lys	Gln	Ile	
225					230					235					240	
Ser	Gly	Phe	Gly	Lys	Lys	Phe	Tyr	Tyr	Lys	Ala	Thr	Val	Met	Phe	Glu	
				245					250					255		
Cys	Asp	Lys	Gly	Phe	Tyr	Leu	Asp	Gly	Ser	Asp	Thr	Ile	Val	Cys	Asp	
		260						265					270			
Ser	Asn	Ser	Thr	Trp	Asp	Pro	Pro	Val	Pro	Lys	Cys	Leu	Lys	Val	Ser	
	275					280						285				
Thr	Ser	Ser	Thr	Thr	Lys	Ser	Pro	Ala	Ser	Ser	Ala	Ser	Gly	Pro	Arg	
	290				295						300					
Pro	Thr	Tyr	Lys	Pro	Pro	Val	Ser	Asn	Tyr	Pro	Gly	Tyr	Pro	Lys	Pro	
305				310						315					320	
Glu	Glu	Gly	Ile	Leu	Asp	Ser	Leu	Asp	Val	Trp	Val	Ile	Ala	Val	Ile	
			325						330					335		
Val	Ile	Ala	Ile	Val	Val	Gly	Val	Ala	Val	Ile	Cys	Val	Val	Pro	Tyr	
	340						345					350				
Arg	Tyr	Leu	Gln	Arg	Arg	Lys	Lys	Gly	Thr	Tyr	Leu	Thr	Asp	Glu		
	355					360					365					
Thr	His	Arg	Glu	Val	Lys	Phe	Thr	Ser	Leu							
	370					375										

<210> 17

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 17

Met	Glu	Val	Ser	Ser	Arg	Ser	Ser	Glu	Pro	Leu	Asp	Pro	Val	Trp	Leu	
1			5					10					15			
Leu	Val	Ala	Phe	Gly	Arg	Gly	Gly	Val	Lys	Leu	Glu	Val	Leu	Leu	Leu	
		20					25					30				
Phe	Leu	Leu	Pro	Phe	Thr	Leu	Gly	His	Cys	Pro	Ala	Pro	Ser	Gln	Leu	
	35					40					45					
Pro	Ser	Ala	Lys	Pro	Ile	Asn	Leu	Thr	Asp	Glu	Ser	Met	Phe	Pro	Ile	
	50					55					60					

Gly	Thr	Tyr	Leu	Leu	Tyr	Glu	Cys	Leu	Pro	Gly	Tyr	Ile	Lys	Arg	Gln	65	70	75	80
Phe	Ser	Ile	Thr	Cys	Lys	Gln	Asp	Ser	Thr	Trp	Thr	Ser	Ala	Glu	Asp	85	90	95	
Lys	Cys	Ile	Arg	Lys	Gln	Cys	Lys	Thr	Pro	Ser	Asp	Pro	Glu	Asn	Gly	100	105	110	
Leu	Val	His	Val	His	Thr	Gly	Ile	Gln	Phe	Gly	Ser	Arg	Ile	Asn	Tyr	115	120	125	
Thr	Cys	Asn	Gln	Gly	Tyr	Arg	Leu	Ile	Gly	Ser	Ser	Ala	Val	Cys		130	135	140	
Val	Ile	Thr	Asp	Gln	Ser	Val	Asp	Trp	Asp	Thr	Glu	Ala	Pro	Ile	Cys	145	150	155	160
Glu	Trp	Ile	Pro	Cys	Glu	Ile	Pro	Pro	Gly	Ile	Pro	Asn	Gly	Asp	Phe	165	170	175	
Phe	Ser	Ser	Thr	Arg	Glu	Asp	Phe	His	Tyr	Gly	Met	Val	Val	Thr	Tyr	180	185	190	
Arg	Cys	Asn	Thr	Asp	Ala	Arg	Gly	Lys	Ala	Leu	Phe	Asn	Leu	Val	Gly	195	200	205	
Glu	Pro	Ser	Leu	Tyr	Cys	Thr	Ser	Asn	Asp	Gly	Glu	Ile	Gly	Val	Trp	210	215	220	
Ser	Gly	Pro	Pro	Pro	Gln	Cys	Ile	Glu	Leu	Asn	Lys	Cys	Thr	Pro	Pro	225	230	235	240
Pro	Tyr	Val	Glu	Asn	Ala	Val	Met	Leu	Ser	Glu	Asn	Arg	Ser	Leu	Phe	245	250	255	
Ser	Leu	Arg	Asp	Ile	Val	Glu	Phe	Arg	Cys	His	Pro	Gly	Phe	Ile	Met	260	265	270	
Lys	Gly	Ala	Ser	Ser	Val	His	Cys	Gln	Ser	Leu	Asn	Lys	Trp	Glu	Pro	275	280	285	
Glu	Leu	Pro	Ser	Cys	Phe	Lys	Gly	Val	Ile	Cys	Arg	Leu	Pro	Gln	Glu	290	295	300	
Met	Ser	Gly	Phe	Gln	Lys	Gly	Leu	Gly	Met	Lys	Lys	Glu	Tyr	Tyr	Tyr	305	310	315	320
Gly	Glu	Asn	Val	Thr	Leu	Glu	Cys	Glu	Asp	Gly	Tyr	Thr	Leu	Glu	Gly	325	330	335	
Ser	Ser	Gln	Ser	Gln	Cys	Gln	Ser	Asp	Gly	Ser	Trp	Asn	Pro	Leu	Leu	340	345	350	
Ala	Lys	Cys	Val	Ser	Arg	Ser	Ile	Ser	Gly	Leu	Ile	Val	Gly	Ile	Phe	355	360	365	
Ile	Gly	Ile	Ile	Val	Phe	Ile	Leu	Val	Ile	Ile	Val	Phe	Ile	Trp	Met	370	375	380	
Ile	Leu	Lys	Tyr	Lys	Lys	Arg	Asn	Thr	Thr	Asp	Glu	Lys	Tyr	Lys	Glu	385	390	395	400
Val	Gly	Ile	His	Leu	Asn	Tyr	Lys	Glu	Asp	Ser	Cys	Val	Arg	Leu	Gln	405	410	415	
Ser	Leu	Leu	Thr	Ser	Gln	Glu	Asn	Ser	Ser	Thr	Thr	Ser	Pro	Ala	Arg	420	425	430	
Asn	Ser	Leu	Thr	Gln	Glu	Val	Ser									435	440		

<210> 18

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 18

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

1				5					10					15			
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro		
			20					25					30				
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val		
		35					40					45					
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val		
		50				55					60						
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln		
65					70					75					80		
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln		
				85					90					95			
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala		
			100					105					110				
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro		
		115					120					125					
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr		
		130				135					140						
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser		
145					150					155					160		
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr		
			165						170					175			
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Pro	Phe	Phe	Leu	Tyr		
		180					185					190					
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe		
		195				200						205					
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys		
		210				215					220						
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys										
225					230												

<210> 19

<211> 454.

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 19

Gly	Ser	Ala	Ser	Ala	Pro	Thr	Leu	Phe	Pro	Leu	Val	Ser	Cys	Glu	Asn		
1				5				10					15				
Ser	Pro	Ser	Asp	Thr	Ser	Ser	Val	Ala	Val	Gly	Cys	Leu	Ala	Gln	Asp		
		20					25					30					
Phe	Leu	Pro	Asp	Ser	Ile	Thr	Phe	Ser	Trp	Lys	Tyr	Lys	Asn	Asn	Ser		
		35				40					45						
Asp	Ile	Ser	Ser	Thr	Arg	Gly	Phe	Pro	Ser	Val	Leu	Arg	Gly	Gly	Lys		
		50				55				60							
Tyr	Ala	Ala	Thr	Ser	Gln	Val	Leu	Leu	Pro	Ser	Lys	Asp	Val	Met	Gln		
65					70					75					80		
Gly	Thr	Asp	Glu	His	Val	Val	Cys	Lys	Val	Gln	His	Pro	Asn	Gly	Asn		
				85					90					95			
Lys	Glu	Lys	Asn	Val	Pro	Leu	Pro	Val	Ile	Ala	Glu	Leu	Pro	Pro	Lys		
		100					105						110				
Val	Ser	Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Phe	Gly	Asn	Pro	Arg		
		115					120					125					
Ser	Lys	Ser	Lys	Leu	Ile	Cys	Gln	Ala	Thr	Gly	Phe	Ser	Pro	Arg	Gln		
		130				135					140						
Ile	Gln	Val	Ser	Trp	Leu	Arg	Glu	Gly	Lys	Gln	Val	Gly	Ser	Gly	Val		
145					150					155					160		


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tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaacttt 720
ttctgtgatg aagggtatcg actgcaaggc ccaccttcta gtcggtgtgt aattgctgga 780
cagggaagt gcttggaacaa aatgccagta tgtgaagaaa ttttttgccc actgcggccg 840
cagtctagag acaaaactca cacatgcccc ccgtgcccag cacctgaact cctgggggga 900
ccgtcagtct tctcttcccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctc 960
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 1020
tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgcgggagga gcagtacaac 1080
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1140
gagtacaagt gcaagggtctc caacaaagcc ctcccagtc ccatcgagaa aaccatctcc 1200
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag 1260
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1320
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1380
ctggactccg acggctcctt cttctcttat agcaagctca ccgtggacaa gagcaggtgg 1440
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1500
cagaagagcc tctccctgtc cccgggtaaa 1530

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<210> 21

<211> 510

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 21

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Met Gly Ala Ala Gly Leu Leu Gly Val Phe Leu Ala Leu Val Ala Pro
 1          5          10          15
Gly Val Leu Gly Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly
          20          25          30
Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
          35          40          45
Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
          50          55          60
Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
65          70          75          80
Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
          85          90          95
Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
          100          105          110
Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
          115          120          125
Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
          130          135          140
Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
145          150          155          160

His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
          165          170          175
Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
          180          185          190
Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
          195          200          205
Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
          210          215          220
Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
225          230          235          240
Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
          245          250          255
Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu
          260          265          270

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Glu Ile Phe Cys Pro Leu Arg Pro Gln Ser Arg Asp Lys Thr His Thr
 275 280 285
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 290 295 300
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 305 310 315 320
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 325 330 335
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 340 345 350
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 355 360 365
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 370 375 380
 Lys Val Ser Asn Lys Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser
 385 390 395 400
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 405 410 415
 Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 420 425 430
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 435 440 445
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 450 455 460
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 465 470 475 480
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 485 490 495
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 500 505 510

<210> 22

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 22

Glu Pro Arg Ile Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Cys Pro
 1 5 10 15
 Pro Gly Asn Ile Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
 20 25 30
 Pro Lys Asp Ala Leu Met Ile Ser Leu Thr Pro Lys Val Thr Cys Val
 35 40 45
 Val Val Asp Val Ser Glu Asp Asp Pro Asp Val His Val Ser Trp Phe
 50 55 60
 Val Asp Asn Lys Glu Val His Thr Ala Trp Thr Gln Pro Arg Glu Ala
 65 70 75 80
 Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Ala Leu Pro Ile Gln His
 85 90 95
 Gln Asp Trp Met Arg Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
 100 105 110
 Ala Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Arg
 115 120 125
 Ala Gln Thr Pro Gln Val Tyr Thr Ile Pro Pro Pro Arg Glu Gln Met
 130 135 140
 Ser Lys Lys Lys Val Ser Leu Thr Cys Leu Val Thr Asn Phe Phe Ser

145		150		155		160									
Glu	Ala	Ile	Ser	Val	Glu	Trp	Glu	Arg	Asn	Gly	Glu	Leu	Glu	Gln	Asp
		165							170					175	
Tyr	Lys	Asn	Thr	Pro	Pro	Ile	Leu	Asp	Ser	Asp	Gly	Thr	Tyr	Phe	Leu
		180						185					190		
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Thr	Asp	Ser	Trp	Leu	Gln	Gly	Glu	Ile
		195				200					205				
Phe	Thr	Cys	Ser	Val	Val	His	Glu	Ala	Leu	His	Asn	His	His	Thr	Gln
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<210> 23

<211> 4860

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 23

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<210> 24

<211> 1620

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 24

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Asp Ile Phe Val His Asp Phe Pro Arg Lys Gln Lys Thr Leu Phe Gln
 35             40             45

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Thr	Arg	Val	Asp	Met	Asn	Pro	Ala	Gly	Gly	Met	Leu	Val	Thr	Pro	Thr
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Ile	Glu	Ile	Pro	Ala	Lys	Glu	Val	Ser	Thr	Asp	Ser	Arg	Gln	Asn	Gln
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Tyr	Val	Val	Val	Gln	Val	Thr	Gly	Pro	Gln	Val	Arg	Leu	Glu	Lys	Val
				85					90					95	
Val	Leu	Leu	Ser	Tyr	Gln	Ser	Ser	Phe	Leu	Phe	Ile	Gln	Thr	Asp	Lys
			100					105					110		
Gly	Ile	Tyr	Thr	Pro	Gly	Ser	Pro	Val	Leu	Tyr	Arg	Val	Phe	Ser	Met
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Asp	His	Asn	Thr	Ser	Lys	Met	Asn	Lys	Thr	Val	Ile	Val	Glu	Phe	Gln
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Thr	Pro	Glu	Gly	Ile	Leu	Val	Ser	Ser	Asn	Ser	Val	Asp	Leu	Asn	Phe
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Phe	Trp	Pro	Tyr	Asn	Leu	Pro	Asp	Leu	Val	Ser	Leu	Gly	Thr	Trp	Arg
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Ile	Val	Ala	Lys	Tyr	Glu	His	Ser	Pro	Glu	Asn	Tyr	Thr	Ala	Tyr	Phe
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Asp	Val	Arg	Lys	Tyr	Val	Leu	Pro	Ser	Phe	Glu	Val	Arg	Leu	Gln	Pro
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Ser	Glu	Lys	Phe	Phe	Tyr	Ile	Asp	Gly	Asn	Glu	Asn	Phe	His	Val	Ser
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Ile	Thr	Ala	Arg	Tyr	Leu	Tyr	Gly	Glu	Glu	Val	Glu	Gly	Val	Ala	Phe
225					230					235					240
Val	Leu	Phe	Gly	Val	Lys	Ile	Asp	Asp	Ala	Lys	Lys	Ser	Ile	Pro	Asp
				245					250					255	
Ser	Leu	Thr	Arg	Ile	Pro	Ile	Ile	Asp	Gly	Asp	Gly	Lys	Ala	Thr	Leu
			260					265					270		
Lys	Arg	Asp	Thr	Phe	Arg	Ser	Arg	Phe	Pro	Asn	Leu	Asn	Glu	Leu	Val
		275					280					285			
Gly	His	Thr	Leu	Tyr	Ala	Ser	Val	Thr	Val	Met	Thr	Glu	Ser	Gly	Ser
		290				295					300				
Asp	Met	Val	Val	Thr	Glu	Gln	Ser	Gly	Ile	His	Ile	Val	Ala	Ser	Pro
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Tyr	Gln	Ile	His	Phe	Thr	Lys	Thr	Pro	Lys	Tyr	Phe	Lys	Pro	Gly	Met
				325					330					335	
Pro	Tyr	Glu	Leu	Thr	Val	Tyr	Val	Thr	Asn	Pro	Asp	Gly	Ser	Pro	Ala
			340					345					350		
Ala	His	Val	Pro	Val	Val	Ser	Glu	Ala	Phe	His	Ser	Met	Gly	Thr	Thr
		355					360					365			
Leu	Ser	Asp	Gly	Thr	Ala	Lys	Leu	Ile	Leu	Asn	Ile	Pro	Leu	Asn	Ala
		370				375					380				
Gln	Ser	Leu	Pro	Ile	Thr	Val	Arg	Thr	Asn	His	Gly	Asp	Leu	Pro	Arg
385					390					395					400
Glu	Arg	Gln	Ala	Thr	Lys	Ser	Met	Thr	Ala	Ile	Ala	Tyr	Gln	Thr	Gln
				405					410					415	
Gly	Gly	Ser	Gly	Asn	Tyr	Leu	His	Val	Ala	Ile	Thr	Ser	Thr	Glu	Ile
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Lys	Pro	Gly	Asp	Asn	Leu	Pro	Val	Asn	Phe	Asn	Val	Lys	Gly	Asn	Ala
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Asn	Ser	Leu	Lys	Gln	Ile	Lys	Tyr	Phe	Thr	Tyr	Leu	Ile	Leu	Asn	Lys
		450				455					460				
Gly	Lys	Ile	Phe	Lys	Val	Gly	Arg	Gln	Pro	Arg	Arg	Asp	Gly	Gln	Asn
465					470					475					480
Leu	Val	Thr	Met	Asn	Leu	His	Ile	Thr	Pro	Asp	Leu	Ile	Pro	Ser	Phe
				485					490					495	
Arg	Phe	Val	Ala	Tyr	Tyr	Gln	Val	Gly	Asn	Asn	Glu	Ile	Val	Ala	Asp
			500					505					510		
Ser	Val	Trp	Val	Asp	Val	Lys	Asp	Thr	Cys	Met	Gly	Thr	Leu	Val	Val
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Lys	Gly	Asp	Asn	Leu	Ile	Gln	Met	Pro	Gly	Ala	Ala	Met	Lys	Ile	Lys

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Leu	Glu	Gly	Asp	Pro	Gly	Ala	Arg	Val	Gly	Leu	Val	Ala	Val	Asp	Lys
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Ala	Val	Tyr	Val	Leu	Asn	Asp	Lys	Tyr	Lys	Ile	Ser	Gln	Ala	Lys	Ile
				565					570						575
Trp	Asp	Thr	Ile	Glu	Lys	Ser	Asp	Phe	Gly	Cys	Thr	Ala	Gly	Ser	Gly
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Gln	Asn	Asn	Leu	Gly	Val	Phe	Glu	Asp	Ala	Gly	Leu	Ala	Leu	Thr	Thr
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Ser	Thr	Asn	Leu	Asn	Thr	Lys	Gln	Arg	Ser	Ala	Ala	Lys	Cys	Pro	Gln
	610					615					620				
Pro	Ala	Asn	Arg	Arg	Arg	Arg	Ser	Ser	Val	Leu	Leu	Leu	Asp	Ser	Asn
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Ala	Ser	Lys	Ala	Ala	Glu	Phe	Gln	Asp	Gln	Asp	Leu	Arg	Lys	Cys	Cys
			645						650						655
Glu	Asp	Val	Met	His	Glu	Asn	Pro	Met	Gly	Tyr	Thr	Cys	Glu	Lys	Arg
	660							665					670		
Ala	Lys	Tyr	Ile	Gln	Glu	Gly	Asp	Ala	Cys	Lys	Ala	Ala	Phe	Leu	Glu
	675					680						685			
Cys	Cys	Arg	Tyr	Ile	Lys	Gly	Val	Arg	Asp	Glu	Asn	Gln	Arg	Glu	Ser
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Glu	Leu	Phe	Leu	Ala	Arg	Asp	Asp	Asn	Glu	Asp	Gly	Phe	Ile	Ala	Asp
705				710					715						720
Ser	Asp	Ile	Ile	Ser	Arg	Ser	Asp	Phe	Pro	Lys	Ser	Trp	Leu	Trp	Leu
			725						730						735
Thr	Lys	Asp	Leu	Thr	Glu	Glu	Pro	Asn	Ser	Gln	Gly	Ile	Ser	Ser	Lys
	740							745					750		
Thr	Met	Ser	Phe	Tyr	Leu	Arg	Asp	Ser	Ile	Thr	Thr	Trp	Val	Val	Leu
	755						760					765			
Ala	Val	Ser	Phe	Thr	Pro	Thr	Lys	Gly	Ile	Cys	Val	Ala	Glu	Pro	Tyr
	770					775					780				
Glu	Ile	Arg	Val	Met	Lys	Val	Phe	Phe	Ile	Asp	Leu	Gln	Met	Pro	Tyr
785				790					795						800
Ser	Val	Val	Lys	Asn	Glu	Gln	Val	Glu	Ile	Arg	Ala	Ile	Leu	His	Asn
			805						810						815
Tyr	Val	Asn	Glu	Asp	Ile	Tyr	Val	Arg	Val	Glu	Leu	Leu	Tyr	Asn	Pro
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Ala	Phe	Cys	Ser	Ala	Ser	Thr	Lys	Gly	Gln	Arg	Tyr	Arg	Gln	Gln	Phe
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Pro	Ile	Lys	Ala	Leu	Ser	Ser	Arg	Ala	Val	Pro	Phe	Val	Ile	Val	Pro
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Leu	Glu	Gln	Gly	Leu	His	Asp	Val	Glu	Ile	Lys	Ala	Ser	Val	Gln	Glu
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Ala	Leu	Trp	Ser	Asp	Gly	Val	Arg	Lys	Lys	Leu	Lys	Val	Val	Pro	Glu
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Gly	Val	Gln	Lys	Ser	Ile	Val	Thr	Ile	Val	Lys	Leu	Asp	Pro	Arg	Ala
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Lys	Gly	Val	Gly	Gly	Thr	Gln	Leu	Glu	Val	Ile	Lys	Ala	Arg	Lys	Leu
	915					920						925			
Asp	Asp	Arg	Val	Pro	Asp	Thr	Glu	Ile	Glu	Thr	Lys	Ile	Ile	Ile	Gln
	930					935					940				
Gly	Asp	Pro	Val	Ala	Gln	Ile	Ile	Glu	Asn	Ser	Ile	Asp	Gly	Ser	Lys
945				950					955						960
Leu	Asn	His	Leu	Ile	Ile	Thr	Pro	Ser	Gly	Cys	Gly	Glu	Gln	Asn	Met
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Ile	Arg	Met	Ala	Ala	Pro	Val	Ile	Ala	Thr	Tyr	Tyr	Leu	Asp	Thr	Thr
	980							985					990		
Glu	Gln	Trp	Glu	Thr	Leu	Gly	Ile	Asn	Arg	Arg	Thr	Glu	Ala	Val	Asn
	995					1000						1005			
Gln	Ile	Val	Thr	Gly	Tyr	Ala	Gln	Gln	Met	Val	Tyr	Lys	Lys	Ala	Asp

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Ile Ser His Glu Ile Ile Cys Gly Gly Val Arg Trp Leu Ile Leu Asn		1055
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Arg Gln Gln Pro Asp Gly Ala Phe Lys Glu Asn Ala Pro Val Leu Ser		1070
	1075	1080
Gly Thr Met Gln Gly Gly Ile Gln Gly Ala Glu Glu Glu Val Tyr Leu		1085
	1090	1095
Thr Ala Phe Ile Leu Val Ala Leu Leu Glu Ser Lys Thr Ile Cys Asn		1100
	1105	1110
Asp Tyr Val Asn Ser Leu Asp Ser Ser Ile Lys Lys Ala Thr Asn Tyr		1115
	1125	1130
Leu Leu Lys Lys Tyr Glu Lys Leu Gln Arg Pro Tyr Thr Thr Ala Leu		1135
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Thr Ala Tyr Ala Leu Ala Ala Ala Asp Gln Leu Asn Asp Arg Val		1150
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Leu Met Ala Ala Ser Thr Gly Arg Asp His Trp Glu Glu Tyr Asn Ala		1165
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His Thr His Asn Ile Glu Gly Thr Ser Tyr Ala Leu Leu Ala Leu Leu		1180
	1185	1190
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Asp Gln Asn Phe Tyr Gly Glu Thr Tyr Gly Gln Thr Gln Ala Thr Val		1215
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Met Ala Phe Gln Ala Leu Ala Glu Tyr Glu Ile Gln Met Pro Thr His		1230
	1235	1240
Lys Asp Leu Asn Leu Asp Ile Thr Ile Glu Leu Pro Asp Arg Glu Val		1245
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Pro Ile Arg Tyr Arg Ile Asn Tyr Glu Asn Ala Leu Leu Ala Arg Thr		1260
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Val Glu Thr Lys Leu Asn Gln Asp Ile Thr Val Thr Ala Ser Gly Asp		1275
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Gly Lys Ala Thr Met Thr Ile Leu Thr Phe Tyr Asn Ala Gln Leu Gln		1295
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Arg Leu Ser Lys Gly Val Asp Arg Tyr Ile Ser Arg Tyr Glu Val Asp		1375
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Asn Asn Met Ala Gln Lys Val Ala Val Ile Ile Tyr Leu Asn Lys Val		1390
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Ser His Ser Glu Asp Glu Cys Leu His Phe Lys Ile Leu Lys His Phe		1405
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Glu Val Gly Phe Ile Gln Pro Gly Ser Val Lys Val Tyr Ser Tyr Tyr		1420
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Glu Thr Cys Ser Ser Leu Asn His Gln Glu Arg Ile Asp Val Pro Leu		1470
	1475	1480
Gln Ile Glu Lys Ala Cys Glu Thr Asn Val Asp Tyr Val Tyr Lys Thr		1485

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Lys Leu Leu Arg Ile Glu Glu Gln Asp Gly Asn Asp Ile Tyr Val Met				
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Asp Val Leu Glu Val Ile Lys Gln Gly Thr Asp Glu Asn Pro Arg Ala				1520
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Lys Thr His Gln Tyr Ile Ser Gln Arg Lys Cys Gln Glu Ala Leu Asn				
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Leu Lys Val Asn Asp Asp Tyr Leu Ile Trp Gly Ser Arg Ser Asp Leu				
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Leu Pro Thr Lys Asp Lys Ile Ser Tyr Ile Ile Thr Lys Asn Thr Trp				
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Ile Glu Arg Trp Pro His Glu Asp Glu Cys Gln Glu Glu Glu Phe Gln				
1585		1590		1595
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 <211> 3039
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
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<210> 26

<211> 1033

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 26

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          20          25          30
Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
      35          40          45
Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
      50          55          60
Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
65          70          75          80
Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
          85          90          95
Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
          100         105         110
Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
      115         120         125
Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
      130         135         140
Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
145          150          155          160
His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
          165          170          175
Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
      180         185         190
Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
      195         200         205
Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
      210         215         220
Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
225          230          235          240
Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys

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Val	Ile	Ala	Gly	245	Gln	Gly	Val	Ala	Trp	250	Thr	Lys	Met	Pro	Val	255	Cys	Glu
			260						265							270		
Glu	Ile	Phe	Cys	Pro	Ser	Pro	Pro	Pro	Pro	Ile	Leu	Asn	Gly	Arg	His	Ile		
		275					280						285					
Gly	Asn	Ser	Leu	Ala	Asn	Val	Ser	Tyr	Gly	Ser	Ile	Val	Thr	Tyr	Thr			
		290				295					300							
Cys	Asp	Pro	Asp	Pro	Glu	Glu	Gly	Val	Asn	Phe	Ile	Leu	Ile	Gly	Glu			
305					310					315					320			
Ser	Thr	Leu	Arg	Cys	Thr	Val	Asp	Ser	Gln	Lys	Thr	Gly	Thr	Trp	Ser			
				325					330					335				
Gly	Pro	Ala	Pro	Arg	Cys	Glu	Leu	Ser	Thr	Ser	Ala	Val	Gln	Cys	Pro			
		340						345					350					
His	Pro	Gln	Ile	Leu	Arg	Gly	Arg	Met	Val	Ser	Gly	Gln	Lys	Asp	Arg			
		355				360						365						
Tyr	Thr	Tyr	Asn	Asp	Thr	Val	Ile	Phe	Ala	Cys	Met	Phe	Gly	Phe	Thr			
		370				375					380							
Leu	Lys	Gly	Ser	Lys	Gln	Ile	Arg	Cys	Asn	Ala	Gln	Gly	Thr	Trp	Glu			
385					390					395					400			
Pro	Ser	Ala	Pro	Val	Cys	Glu	Lys	Glu	Cys	Gln	Ala	Pro	Pro	Asn	Ile			
				405					410					415				
Leu	Asn	Gly	Gln	Lys	Glu	Asp	Arg	His	Met	Val	Arg	Phe	Asp	Pro	Gly			
			420					425					430					
Thr	Ser	Ile	Lys	Tyr	Ser	Cys	Asn	Pro	Gly	Tyr	Val	Leu	Val	Gly	Glu			
		435					440					445						
Glu	Ser	Ile	Gln	Cys	Thr	Ser	Glu	Gly	Val	Trp	Thr	Pro	Pro	Val	Pro			
		450				455					460							
Gln	Cys	Lys	Val	Ala	Ala	Cys	Glu	Ala	Thr	Gly	Arg	Gln	Leu	Leu	Thr			
465					470					475					480			
Lys	Pro	Gln	His	Gln	Phe	Val	Arg	Pro	Asp	Val	Asn	Ser	Ser	Cys	Gly			
				485					490					495				
Glu	Gly	Tyr	Lys	Leu	Ser	Gly	Ser	Val	Tyr	Gln	Glu	Cys	Gln	Gly	Thr			
			500					505					510					
Ile	Pro	Trp	Phe	Met	Glu	Ile	Arg	Leu	Cys	Lys	Glu	Ile	Thr	Cys	Pro			
		515					520					525						
Pro	Pro	Pro	Val	Ile	Tyr	Asn	Gly	Ala	His	Thr	Gly	Ser	Ser	Leu	Glu			
		530				535					540							
Asp	Phe	Pro	Tyr	Gly	Thr	Val	Thr	Tyr	Thr	Cys	Asn	Pro	Gly	Pro				
545					550					555				560				
Glu	Arg	Gly	Val	Glu	Phe	Ser	Leu	Ile	Gly	Glu	Ser	Thr	Ile	Arg	Cys			
				565					570					575				
Thr	Ser	Asn	Asp	Gln	Glu	Arg	Gly	Thr	Trp	Ser	Gly	Pro	Ala	Pro	Leu			
			580					585					590					
Cys	Lys	Leu	Ser	Leu	Leu	Ala	Val	Gln	Cys	Ser	His	Val	His	Ile	Ala			
		595				600						605						
Asn	Gly	Tyr	Lys	Ile	Ser	Gly	Lys	Glu	Ala	Pro	Tyr	Phe	Tyr	Asn	Asp			
		610				615						620						
Thr	Val	Thr	Phe	Lys	Cys	Tyr	Ser	Gly	Phe	Thr	Leu	Lys	Gly	Ser	Ser			
625					630					635					640			
Gln	Ile	Arg	Cys	Lys	Ala	Asp	Asn	Thr	Trp	Asp	Pro	Glu	Ile	Pro	Val			
				645					650					655				
Cys	Glu	Lys	Glu	Thr	Cys	Gln	His	Val	Arg	Gln	Ser	Leu	Gln	Glu	Leu			
			660					665					670					
Pro	Ala	Gly	Ser	Arg	Val	Glu	Leu	Val	Asn	Thr	Ser	Cys	Gln	Asp	Gly			
		675				680						685						
Tyr	Gln	Leu	Thr	Gly	His	Ala	Tyr	Gln	Met	Cys	Gln	Asp	Ala	Glu	Asn			
		690				695					700							
Gly	Ile	Trp	Phe	Lys	Lys	Ile	Pro	Leu	Cys	Lys	Val	Ile	His	Cys	His			
705					710					715				720				
Pro	Pro	Pro	Val	Ile	Val	Asn	Gly	Lys	His	Thr	Gly	Met	Met	Ala	Glu			
				725					730					735				

Asn	Phe	Leu	Tyr	Gly	Asn	Glu	Val	Ser	Tyr	Glu	Cys	Asp	Gln	Gly	Phe	
		740						745					750			
Tyr	Leu	Leu	Gly	Glu	Lys	Lys	Leu	Gln	Cys	Arg	Ser	Asp	Ser	Lys	Gly	
		755					760					765				
His	Gly	Ser	Trp	Ser	Gly	Pro	Ser	Pro	Gln	Cys	Leu	Arg	Ser	Pro	Pro	
		770				775					780					
Val	Thr	Arg	Cys	Pro	Asn	Pro	Glu	Val	Lys	His	Gly	Tyr	Lys	Leu	Asn	
		785			790					795					800	
Lys	Thr	His	Ser	Ala	Tyr	Ser	His	Asn	Asp	Ile	Val	Tyr	Val	Asp	Cys	
			805						810					815		
Asn	Pro	Gly	Phe	Ile	Met	Asn	Gly	Ser	Arg	Val	Ile	Arg	Cys	His	Thr	
		820						825					830			
Asp	Asn	Thr	Trp	Val	Pro	Gly	Val	Pro	Thr	Cys	Met	Lys	Lys	Ala	Phe	
		835					840					845				
Ile	Gly	Cys	Pro	Pro	Pro	Pro	Lys	Thr	Pro	Asn	Gly	Asn	His	Thr	Gly	
		850				855					860					
Gly	Asn	Ile	Ala	Arg	Phe	Ser	Pro	Gly	Met	Ser	Ile	Leu	Tyr	Ser	Cys	
		865			870				875						880	
Asp	Gln	Gly	Tyr	Leu	Leu	Val	Gly	Glu	Ala	Leu	Leu	Leu	Cys	Thr	His	
			885					890						895		
Glu	Gly	Thr	Trp	Ser	Gln	Pro	Ala	Pro	His	Cys	Lys	Glu	Val	Asn	Cys	
		900						905					910			
Ser	Ser	Pro	Ala	Asp	Met	Asp	Gly	Ile	Gln	Lys	Gly	Leu	Glu	Pro	Arg	
		915					920					925				
Lys	Met	Tyr	Gln	Tyr	Gly	Ala	Val	Val	Thr	Leu	Glu	Cys	Glu	Asp	Gly	
		930			935						940					
Tyr	Met	Leu	Glu	Gly	Ser	Pro	Gln	Ser	Gln	Cys	Gln	Ser	Asp	His	Gln	
		945			950					955					960	
Trp	Asn	Pro	Pro	Leu	Ala	Val	Cys	Arg	Ser	Arg	Ser	Leu	Ala	Pro	Val	
			965					970						975		
Leu	Cys	Gly	Ile	Ala	Ala	Gly	Leu	Ile	Leu	Leu	Thr	Phe	Leu	Ile	Val	
		980						985					990			
Ile	Thr	Leu	Tyr	Val	Ile	Ser	Lys	His	Arg	Glu	Arg	Asn	Tyr	Tyr	Thr	
		995				1000						1005				
Asp	Thr	Ser	Gln	Lys	Glu	Ala	Phe	His	Leu	Glu	Ala	Arg	Glu	Val	Tyr	
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Ser	Val	Asp	Pro	Tyr	Asn	Pro	Ala	Ser								
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<210> 27

<211> 3042

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 27

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aaggctatct tttgtataag tgaaaatcaa gtgcatgcca cctgggataa agctcctcct 180
atatgtgaat ctgtgaataa aaccatttct tgctcagatc ccatagtagc agggggattc 240
atgaataaag gatctaaggc accattcaga catggtgatt ctgtgacatt tacctgtaaa 300
gccaacttca ccatgaaagg aagcaaaact gtctggtgcc aggcaaatga aatgtgggga 360
ccaacagctc tgccagctcg tgagagtgat ttccctctgg agtgcccatc acttccaacg 420
attcataatg gacaccacac aggacagcat ttgaccagt ttgttgctgg gttgtctgtg 480
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tcaggagact gggatggtgt catcccgaca tgcaaagagg cccagtgtga acatccagga 600
aagtttccca atgggcaggt aaaggaacct ctgagccttc aggttggcac aactgtgtac 660

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<210> 28

<211> 1014

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 28

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      20             25             30
Pro Ser Tyr Arg Leu Ile Gly Glu Lys Ala Ile Phe Cys Ile Ser Glu
      35             40             45
Asn Gln Val His Ala Thr Trp Asp Lys Ala Pro Pro Ile Cys Glu Ser
      50             55             60
Val Asn Lys Thr Ile Ser Cys Ser Asp Pro Ile Val Pro Gly Gly Phe

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65					70					75				80
Met	Asn	Lys	Gly	Ser	Lys	Ala	Pro	Phe	Arg	His	Gly	Asp	Ser	Val
				85					90					95
Phe	Thr	Cys	Lys	Ala	Asn	Phe	Thr	Met	Lys	Gly	Ser	Lys	Thr	Val
			100					105					110	
Cys	Gln	Ala	Asn	Glu	Met	Trp	Gly	Pro	Thr	Ala	Leu	Pro	Val	Cys
			115				120					125		
Ser	Asp	Phe	Pro	Leu	Glu	Cys	Pro	Ser	Leu	Pro	Thr	Ile	His	Asn
			130			135					140			
His	His	Thr	Gly	Gln	His	Val	Asp	Gln	Phe	Val	Ala	Gly	Leu	Ser
145					150					155				160
Thr	Tyr	Ser	Cys	Glu	Pro	Gly	Tyr	Leu	Leu	Thr	Gly	Lys	Lys	Thr
			165					170						175
Lys	Cys	Leu	Ser	Ser	Gly	Asp	Trp	Asp	Gly	Val	Ile	Pro	Thr	Cys
			180				185					190		
Glu	Ala	Gln	Cys	Glu	His	Pro	Gly	Lys	Phe	Pro	Asn	Gly	Gln	Val
			195				200					205		
Glu	Pro	Leu	Ser	Leu	Gln	Val	Gly	Thr	Thr	Val	Tyr	Phe	Ser	Cys
			210			215					220			
Glu	Gly	Tyr	Gln	Leu	Gln	Gly	Gln	Pro	Ser	Ser	Gln	Cys	Val	Ile
225					230					235				240
Glu	Gln	Lys	Ala	Ile	Trp	Thr	Lys	Lys	Pro	Val	Cys	Lys	Glu	Ile
			245					250						255
Cys	Pro	Pro	Pro	Pro	Pro	Val	Arg	Asn	Gly	Ser	His	Thr	Gly	Ser
			260				265					270		
Ser	Glu	Asn	Val	Pro	Tyr	Gly	Ser	Thr	Val	Thr	Tyr	Thr	Cys	Asp
			275			280					285			
Ser	Pro	Glu	Lys	Gly	Val	Ser	Phe	Thr	Leu	Ile	Gly	Glu	Lys	Thr
			290			295					300			
Asn	Cys	Thr	Thr	Gly	Ser	Gln	Lys	Thr	Gly	Ile	Trp	Ser	Gly	Pro
305					310					315				320
Pro	Tyr	Cys	Val	Leu	Ser	Thr	Ser	Ala	Val	Leu	Cys	Leu	Gln	Pro
			325					330						335
Ile	Lys	Arg	Gly	Gln	Ile	Leu	Ser	Ile	Leu	Lys	Asp	Ser	Tyr	Ser
			340					345				350		
Asn	Asp	Thr	Val	Ala	Phe	Ser	Cys	Glu	Pro	Gly	Phe	Thr	Leu	Lys
			355			360					365			
Asn	Arg	Ser	Ile	Arg	Cys	Asn	Ala	His	Gly	Thr	Trp	Glu	Pro	Pro
			370			375					380			
Pro	Val	Cys	Glu	Lys	Gly	Cys	Gln	Ala	Pro	Pro	Lys	Ile	Ile	Asn
385					390				395					400
Gln	Lys	Glu	Asp	Ser	Tyr	Leu	Leu	Asn	Phe	Asp	Pro	Gly	Thr	Ser
			405					410						415
Arg	Tyr	Ser	Cys	Asp	Pro	Gly	Tyr	Leu	Leu	Val	Gly	Glu	Asp	Thr
			420				425					430		
His	Cys	Thr	Pro	Glu	Gly	Lys	Trp	Thr	Pro	Ile	Thr	Pro	Gln	Cys
			435			440					445			
Val	Ala	Glu	Cys	Lys	Pro	Val	Gly	Pro	His	Leu	Phe	Lys	Arg	Pro
			450			455					460			
Asn	Gln	Phe	Ile	Arg	Thr	Ala	Val	Asn	Ser	Ser	Cys	Asp	Glu	Gly
465					470				475					480
Gln	Leu	Ser	Glu	Ser	Ala	Tyr	Gln	Leu	Cys	Gln	Gly	Thr	Ile	Pro
			485					490						495
Phe	Ile	Glu	Ile	Arg	Leu	Cys	Lys	Glu	Ile	Thr	Cys	Pro	Pro	Pro
			500				505					510		
Val	Ile	His	Asn	Gly	Thr	His	Thr	Trp	Ser	Ser	Ser	Glu	Asp	Val
			515			520						525		
Tyr	Gly	Thr	Val	Val	Thr	Tyr	Met	Cys	Tyr	Pro	Gly	Pro	Glu	Glu
			530			535					540			
Val	Lys	Phe	Lys	Leu	Ile	Gly	Glu	Gln	Thr	Ile	His	Cys	Thr	Ser
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Ser Arg Gly Arg Gly Ser Trp Ser Ser Pro Ala Pro Leu Cys Lys Leu
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 Ser Leu Pro Ala Val Gln Cys Thr Asp Val His Val Glu Asn Gly Val
 580 585 590
 Lys Leu Thr Asp Asn Lys Ala Pro Tyr Phe Tyr Asn Asp Ser Val Met
 595 600 605
 Phe Lys Cys Asp Asp Gly Tyr Ile Leu Ser Gly Ser Ser Gln Ile Arg
 610 615 620
 Cys Lys Ala Asn Asn Thr Trp Asp Pro Glu Lys Pro Leu Cys Lys Lys
 625 630 635 640
 Glu Gly Cys Glu Pro Met Arg Val His Gly Leu Pro Asp Asp Ser His
 645 650 655
 Ile Lys Leu Val Lys Arg Thr Cys Gln Asn Gly Tyr Gln Leu Thr Gly
 660 665 670
 Tyr Thr Tyr Glu Lys Cys Gln Asn Ala Glu Asn Gly Thr Trp Phe Lys
 675 680 685
 Lys Ile Glu Val Cys Thr Val Ile Leu Cys Gln Pro Pro Pro Lys Ile
 690 695 700
 Ala Asn Gly Gly His Thr Gly Met Met Ala Lys His Phe Leu Tyr Gly
 705 710 715 720
 Asn Glu Val Ser Tyr Glu Cys Asp Glu Gly Phe Tyr Leu Leu Gly Glu
 725 730 735
 Lys Ser Leu Gln Cys Val Asn Asp Ser Lys Gly His Gly Ser Trp Ser
 740 745 750
 Gly Pro Pro Pro Gln Cys Leu Gln Ser Ser Pro Leu Thr His Cys Pro
 755 760 765
 Asp Pro Glu Val Lys His Gly Tyr Lys Leu Asn Lys Thr His Ser Ala
 770 775 780
 Phe Ser His Asn Asp Ile Val His Phe Val Cys Asn Gln Gly Phe Ile
 785 790 795 800
 Met Asn Gly Ser His Leu Ile Arg Cys His Thr Asn Asn Thr Trp Leu
 805 810 815
 Pro Gly Val Pro Thr Cys Ile Arg Lys Ala Ser Leu Gly Cys Gln Ser
 820 825 830
 Pro Ser Thr Ile Pro Asn Gly Asn His Thr Gly Gly Ser Ile Ala Arg
 835 840 845
 Phe Pro Pro Gly Met Ser Val Met Tyr Ser Cys Tyr Gln Gly Phe Leu
 850 855 860
 Met Ala Gly Glu Ala Arg Leu Ile Cys Thr His Glu Gly Thr Trp Ser
 865 870 875 880
 Gln Pro Pro Pro Phe Cys Lys Glu Val Asn Cys Ser Phe Pro Glu Asp
 885 890 895
 Thr Asn Gly Ile Gln Lys Gly Phe Gln Pro Gly Lys Thr Tyr Arg Phe
 900 905 910
 Gly Ala Thr Val Thr Leu Glu Cys Glu Asp Gly Tyr Thr Leu Glu Gly
 915 920 925
 Ser Pro Gln Ser Gln Cys Gln Asp Asp Ser Gln Trp Asn Pro Pro Leu
 930 935 940
 Ala Leu Cys Lys Tyr Arg Arg Trp Ser Thr Ile Pro Leu Ile Cys Gly
 945 950 955 960
 Ile Ser Val Gly Ser Ala Leu Ile Ile Leu Met Ser Val Gly Phe Cys
 965 970 975
 Met Ile Leu Lys His Arg Glu Ser Asn Tyr Tyr Thr Lys Thr Arg Pro
 980 985 990
 Lys Glu Gly Ala Leu His Leu Glu Thr Arg Glu Val Tyr Ser Ile Asp
 995 1000 1005
 Pro Tyr Asn Pro Ala Ser
 1010

<210> 29

<211> 1033
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 29
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 1 5 10 15
 Gly Val Leu Gly Ile Ser Cys Gly Ser Pro Pro Pro Val Leu Asn Gly
 20 25 30
 Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
 35 40 45
 Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
 50 55 60
 Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
 65 70 75 80
 Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
 85 90 95
 Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
 100 105 110
 Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
 115 120 125
 Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
 130 135 140
 Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
 145 150 155 160
 His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
 165 170 175
 Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
 180 185 190
 Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
 195 200 205
 Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
 210 215 220
 Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
 225 230 235 240
 Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
 245 250 255
 Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu
 260 265 270
 Glu Ile Phe Cys Pro Ser Pro Pro Pro Ile Leu Asn Gly Arg His Ile
 275 280 285
 Gly Asn Ser Leu Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr
 290 295 300
 Cys Asp Pro Asp Pro Glu Glu Gly Val Asn Phe Ile Leu Ile Gly Glu
 305 310 315 320
 Ser Thr Leu Arg Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser
 325 330 335
 Gly Pro Ala Pro Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro
 340 345 350
 His Pro Gln Ile Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg
 355 360 365
 Tyr Thr Tyr Asn Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr
 370 375 380
 Leu Lys Gly Ser Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu
 385 390 395 400
 Pro Ser Ala Pro Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile
 405 410 415

Leu	Asn	Gly	Gln	Lys	Glu	Asp	Arg	His	Met	Val	Arg	Phe	Asp	Pro	Gly	420	425	430
Thr	Ser	Ile	Lys	Tyr	Ser	Cys	Asn	Pro	Gly	Tyr	Val	Leu	Val	Gly	Glu	435	440	445
Glu	Ser	Ile	Gln	Cys	Thr	Ser	Glu	Gly	Val	Trp	Thr	Pro	Pro	Val	Pro	450	455	460
Gln	Cys	Lys	Val	Ala	Ala	Cys	Glu	Ala	Thr	Gly	Arg	Gln	Leu	Leu	Thr	465	470	475
Lys	Pro	Gln	His	Gln	Phe	Val	Arg	Pro	Asp	Val	Asn	Ser	Ser	Cys	Gly	485	490	495
Glu	Gly	Tyr	Lys	Leu	Ser	Gly	Ser	Val	Tyr	Gln	Glu	Cys	Gln	Gly	Thr	500	505	510
Ile	Pro	Trp	Phe	Met	Glu	Ile	Arg	Leu	Cys	Lys	Glu	Ile	Thr	Cys	Pro	515	520	525
Pro	Pro	Pro	Val	Ile	Tyr	Asn	Gly	Ala	His	Thr	Gly	Ser	Ser	Leu	Glu	530	535	540
Asp	Phe	Pro	Tyr	Gly	Thr	Thr	Val	Thr	Tyr	Thr	Cys	Asn	Pro	Gly	Pro	545	550	555
Glu	Arg	Gly	Val	Glu	Phe	Ser	Leu	Ile	Gly	Glu	Ser	Thr	Ile	Arg	Cys	565	570	575
Thr	Ser	Asn	Asp	Gln	Glu	Arg	Gly	Thr	Trp	Ser	Gly	Pro	Ala	Pro	Leu	580	585	590
Cys	Lys	Leu	Ser	Leu	Leu	Ala	Val	Gln	Cys	Ser	His	Val	His	Ile	Ala	595	600	605
Asn	Gly	Tyr	Lys	Ile	Ser	Gly	Lys	Glu	Ala	Pro	Tyr	Phe	Tyr	Asn	Asp	610	615	620
Thr	Val	Thr	Phe	Lys	Cys	Tyr	Ser	Gly	Phe	Thr	Leu	Lys	Gly	Ser	Ser	625	630	635
Gln	Ile	Arg	Cys	Lys	Ala	Asp	Asn	Thr	Trp	Asp	Pro	Glu	Ile	Pro	Val	645	650	655
Cys	Glu	Lys	Glu	Thr	Cys	Gln	His	Val	Arg	Gln	Ser	Leu	Gln	Glu	Leu	660	665	670
Pro	Ala	Gly	Ser	Arg	Val	Glu	Leu	Val	Asn	Thr	Ser	Cys	Gln	Asp	Gly	675	680	685
Tyr	Gln	Leu	Thr	Gly	His	Ala	Tyr	Gln	Met	Cys	Gln	Asp	Ala	Glu	Asn	690	695	700
Gly	Ile	Trp	Phe	Lys	Lys	Ile	Pro	Leu	Cys	Lys	Val	Ile	His	Cys	His	705	710	715
Pro	Pro	Pro	Val	Ile	Val	Asn	Gly	Lys	His	Thr	Gly	Met	Met	Ala	Glu	725	730	735
Asn	Phe	Leu	Tyr	Gly	Asn	Glu	Val	Ser	Tyr	Glu	Cys	Asp	Gln	Gly	Phe	740	745	750
Tyr	Leu	Leu	Gly	Glu	Lys	Lys	Leu	Gln	Cys	Arg	Ser	Asp	Ser	Lys	Gly	755	760	765
His	Gly	Ser	Trp	Ser	Gly	Pro	Ser	Pro	Gln	Cys	Leu	Arg	Ser	Pro	Pro	770	775	780
Val	Thr	Arg	Cys	Pro	Asn	Pro	Glu	Val	Lys	His	Gly	Tyr	Lys	Leu	Asn	785	790	795
Lys	Thr	His	Ser	Ala	Tyr	Ser	His	Asn	Asp	Ile	Val	Tyr	Val	Asp	Cys	805	810	815
Asn	Pro	Gly	Phe	Ile	Met	Asn	Gly	Ser	Arg	Val	Ile	Arg	Cys	His	Thr	820	825	830
Asp	Asn	Thr	Trp	Val	Pro	Gly	Val	Pro	Thr	Cys	Met	Lys	Lys	Ala	Phe	835	840	845
Ile	Gly	Cys	Pro	Pro	Pro	Pro	Lys	Thr	Pro	Asn	Gly	Asn	His	Thr	Gly	850	855	860
Gly	Asn	Ile	Ala	Arg	Phe	Ser	Pro	Gly	Met	Ser	Ile	Leu	Tyr	Ser	Cys	865	870	875
Asp	Gln	Gly	Tyr	Leu	Leu	Val	Gly	Glu	Ala	Leu	Leu	Leu	Cys	Thr	His	885	890	895
Glu	Gly	Thr	Trp	Ser	Gln	Pro	Ala	Pro	His	Cys	Lys	Glu	Val	Asn	Cys			

